OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: May 28, 2005, 23:00:05 ; Search time 4174.5 Seconds
                                            (without alignments)
                                            11934,968 Million cell updates/sec

Title: US-09-778-516C-2
Perfect score: 8115
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Scoring table: IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched: 5700845 seqs, 3069779757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	5812.4	71.6	8115	9	US-09-778-516A-1	Sequence 1, Appli
c 3	2115	26.1	8115	9	US-09-778-516A-1	Sequence 1, Appl
4	1567.4	19.3	5155	19	US-10-492-403A-9	Sequence 9, Appli
5	1507	18.6	5175	17	US-10-285-874-14	Sequence 14, Appl
6	1502.4	18.5	5178	17	US-10-285-874-13	Sequence 13, Appl
7	1264.2	15.6	3982	17	US-10-387-252-3	Sequence 3, Appl
8	1223.6	15.1	5308	10	US-09-826-115-15	Sequence 15, Appl
9	1222.6	15.1	5334	10	US-09-826-115-17	Sequence 17, Appl
10	1215.6	15.0	5283	10	US-09-826-115-19	Sequence 19, Appl
11	1215.4	15.0	5271	10	US-09-826-115-23	Sequence 23, Appl

12	1215.4	15.0	5304	10	US-09-826-115-21	Sequence 21, Appl
13	1169.2	14.4	4059	18	US-10-655-702-1	Sequence 1, Appli
14	1152.4	14.2	5314	16	US-10-331-329-27	Sequence 27, Appl
15	1151.6	14.1	5382	16	US-10-331-329-21	Sequence 21, Appl
16	1148.2	14.1	14455	9	US-09-847-101B-15	Sequence 15, Appl
17	1148.2	14.1	14455	10	US-09-482-682-15	Sequence 15, Appl
18	1141.8	14.1	4644	16	US-10-331-329-19	Sequence 19, Appl
19	1109.8	13.7	5247	16	US-10-331-329-20	Sequence 20, Appl
20	1082	13.3	5446	9	US-09-844-645-3	Sequence 3, Appli
21	1082	13.3	5446	9	US-09-559-874-5	Sequence 5, Appli
22	1082	13.3	5446	17	US-10-371-116A-1	Sequence 1, Appli
23	1068	13.2	8705	15	US-10-291-230-14	Sequence 14, Appl
24	1068	13.2	8705	15	US-10-291-249-14	Sequence 14, Appl
25	1068	13.2	8705	17	US-10-273-678-16	Sequence 16, Appl
26	1058.4	13.0	4622	9	US-09-846-091-11	Sequence 11, Appl
27	1058.4	13.0	6050	9	US-09-491-974-4	Sequence 4, Appli
28	1058.4	13.0	6050	17	US-10-394-388A-4	Sequence 4, Appli
29	1056.8	13.0	8001	9	US-09-491-974-3	Sequence 3, Appli
30	1056.8	13.0	8001	17	US-10-394-388A-3	Sequence 3, Appli
31	1053.6	13.0	7807	17	US-10-394-388A-7	Sequence 7, Appli
32	1052	13.0	7913	17	US-10-394-388A-8	Sequence 8, Appli
33	1052	13.0	13464	17	US-10-394-388A-9	Sequence 9, Appli
34	1036.2	12.8	4293	13	US-10-127-391-32	Sequence 32, Appl
35	1036.2	12.8	3796	16	US-10-241-332-32	Sequence 32, Appl
36	1036.2	12.8	3796	15	US-10-277-184-3	Sequence 3, Appli
37	988	12.2	4597	15	US-10-241-332-5	Sequence 5, Appli
38	983	12.1	4058	19	US-10-811-028A-5	Sequence 5, Appli
39	983	12.1	4187	19	US-10-811-028A-6	Sequence 6, Appli
40	983	12.1	4332	19	US-10-811-028A-2	Sequence 2, Appli
41	983	12.1	5753	19	US-10-811-028A-3	Sequence 3, Appli
42	983	12.1	5760	19	US-10-811-028A-4	Sequence 4, Appli
43	981.8	12.1	6565	14	US-10-267-117-1	Sequence 1, Appli
44	981.8	12.1	6565	14	US-10-340-112-1	Sequence 1, Appli
45	981.8	12.1	6981	14	US-10-267-117-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-778-516A-2
Sequence 2, Application US/09778516A
Patent No. US2002010272A1
; GENERAL INFORMATION:
; APPLICANT: Lo, Wei-Yu
; APPLICANT: Lo, Ming Ching
; APPLICANT: Liau, Pei-Ru
; TITLE OF INVENTION: LAC SHUTTLE VECTORS
; FILE REFERENCE: 12875-002001
; CURRENT APPLICATION NUMBER: US/09/778,516A
; CURRENT FILING DATE: 2007-02-07
; PRIOR APPLICATION NUMBER: TW 89110235
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 8115
; TYPE: DNA
; ORGANISM: Lactobacillus plantarum
US-09-778-516A-2

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Qy   61 ATTACGGGGGTCATTAGTTCATTAGCGCCCATATATGAGGTTCCGCGTTACATAACTTACGGGGTA 120
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Db   61 ATTACGGGGGTCATTAGTTCATTAGCGCCCATATATGGAGGTTCCGCGTTACATAACTTACGGGTA 120

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: May 28, 2005, 19:59:45 ; Search time 1161 Seconds
(without alignments)
11437.025 Million cell updates/sec

Title: US-09-778-516C-2
Perfect score: 8115
Sequence: 1 gatgtacgggcccagatatac..........gcgtgtcgctagcgacggtc 8115

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Match Length	DB	ID	Description
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5	1152.4	14.2	5314	3	US-09-481-355-27	Sequence 27, Appl
6	1152.4	14.2	5314	4	US-09-481-282-27	Sequence 27, Appl
7	1152.4	14.2	5314	4	US-09-455-659A-27	Sequence 27, Appl
8	1152.4	14.2	5314	4	US-09-484-996-27	Sequence 27, Appl
9	1152.4	14.2	5314	4	US-09-479-123-27	Sequence 27, Appl
10	1152.4	14.2	5314	3	US-09-484-317A-27	Sequence 27, Appl
11	1151.6	14.2	5382	3	US-09-479-122-21	Sequence 21, Appl
12	1151.6	14.2	5382	4	US-09-484-997-21	Sequence 21, Appl
13	1151.6	14.2	5382	4	US-09-481-355-21	Sequence 21, Appl
14	1151.6	14.2	5382	4	US-09-481-282-21	Sequence 21, Appl
15	1151.6	14.2	5382	4	US-09-455-659A-21	Sequence 21, Appl
16	1151.6	14.2	5382	4	US-09-484-996-21	Sequence 21, Appl
17	1151.6	14.2	5382	4	US-09-479-123-21	Sequence 21, Appl
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20	1141.8	14.1	4644	4	US-09-484-997-19	Sequence 19, Appl
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22	1141.8	14.1	4644	4	US-09-481-282-19	Sequence 19, Appl
23	1141.8	14.1	4644	4	US-09-455-659A-19	Sequence 19, Appl
24	1141.8	14.1	4644	4	US-09-484-996-19	Sequence 19, Appl
25	1141.8	14.1	4644	4	US-09-479-123-19	Sequence 19, Appl
26	1141.8	14.1	4644	4	US-09-484-317A-19	Sequence 19, Appl
27	1109.8	13.7	5247	3	US-09-479-122-20	Sequence 20, Appl
28	1109.8	13.7	5247	4	US-09-484-997-20	Sequence 20, Appl
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30	1109.8	13.7	5247	4	US-09-481-282-20	Sequence 20, Appl
31	1109.8	13.7	5247	4	US-09-455-659A-20	Sequence 20, Appl
32	1109.8	13.7	5247	4	US-09-484-996-20	Sequence 20, Appl
33	1109.8	13.7	5247	4	US-09-479-123-20	Sequence 20, Appl
34	1109.8	13.7	5247	4	US-09-484-317A-20	Sequence 20, Appl
35	1068.6	13.2	4026	3	US-09-801-092-19	Sequence 19, Appl
36	1068.6	13.2	4026	3	US-09-315-113-19	Sequence 19, Appl
37	1068	13.2	8705	4	US-09-647-344A-14	Sequence 14, Appli
38	1053.6	13.0	4326	3	US-08-760-615-7	Sequence 7, Appli
39	1036.2	12.8	3796	4	US-09-470-661A-32	Sequence 32, Appli
40	985.2	12.1	4276	4	US-09-721-480-1	Sequence 1, Appli
41	985.2	12.1	5128	4	US-09-721-480-2	Sequence 2, Appli
42	985.2	12.1	5459	4	US-09-721-480-4	Sequence 4, Appli
43	985.2	12.1	5882	4	US-09-721-480-6	Sequence 6, Appli
44	981.8	12.1	6253	3	US-08-893-327-15	Sequence 15, Appl
45	981.8	12.1	6280	3	US-08-893-327-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-801-092-5
Sequence 5, Application US/08801092
Patent No. 6074850
GENERAL INFORMATION:
; APPLICANT: Antelman, Douglas
; APPLICANT: Gregory, Richard J.
; APPLICANT: Wils, Kenneth N.
; TITLE OF INVENTION: Tissue Specific Expression of
; TITLE OF INVENTION: Retinoblastoma Protein
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,092
; FILING DATE: 14-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/751,517
; FILING DATE: 15-NOV-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 016930-001020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 703-576-0300
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3853 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 209..250
; FEATURE:
; NAME/KEY: CDS

OM nucleic - nucleic search, using sw model

GenCore version 5.1.6
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Run on: May 28, 2005, 23:00:05 ; Search time 4174.5 Seconds (without alignments)
11934.968 Million cell updates/sec

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7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	8115	100.0	8115	9	US-09-778-516A-1	Sequence 1, Appl
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c 3	2215	26.1	9		US-09-778-516A-2	Sequence 2, Appli
4	1567.4	19.3	5155	19	US-10-492-403A-9	Sequence 9, Appli
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6	1502.4	18.5	5175	17	US-10-285-874-13	Sequence 13, Appli
7	1264.2	15.6	3982	17	US-10-387-252-3	Sequence 3, Appli
8	1223.6	15.1	5308	10	US-09-826-115-15	Sequence 15, Appl
9	1222.6	15.1	5334	10	US-09-826-115-17	Sequence 17, Appl
10	1215.6	15.0	5283	10	US-09-826-115-19	Sequence 19, Appl
11	1215.4	15.0	5271	10	US-09-826-115-23	Sequence 23, Appl
12	1215.2	15.0	5304	10	US-09-826-115-21	Sequence 21, Appl
13	1169.2	14.4	4059	18	US-10-655-702-1	Sequence 1, Appli
14	1152.4	14.2	5314	16	US-10-331-329-27	Sequence 27, Appl
15	1151.6	14.2	5382	16	US-10-331-329-21	Sequence 21, Appl
16	1148.2	14.1	14455	9	US-09-847-101B-15	Sequence 15, Appl
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18	1141.8	14.1	4644	16	US-10-331-329-19	Sequence 19, Appl
19	1109.8	13.7	5247	16	US-10-331-329-20	Sequence 20, Appl
20	1082	13.3	8705	15	US-09-844-645-3	Sequence 3, Appli
21	1082	13.3	5446	9	US-09-559-874-5	Sequence 5, Appli
22	1082	13.3	5446	17	US-10-291-230-14	Sequence 14, Appli
23	1068	13.2	8705	15	US-10-291-249-14	Sequence 14, Appl
24	1068	13.2	8705	17	US-10-273-678-16	Sequence 16, Appl
25	1068	13.2	4622	9	US-09-491-974-11	Sequence 11, Appl
26	1058.4	13.0	6050	17	US-09-491-974-3	Sequence 3, Appli
27	1058.4	13.0	6050	15	US-09-491-974-4	Sequence 4, Appli
28	1058.4	13.0	4622	9	US-10-394-388A-4	Sequence 4, Appli
29	1056.8	13.0	8001	15	US-10-394-388A-3	Sequence 3, Appli
30	1056.8	13.0	8001	17	US-09-491-974-3	Sequence 3, Appli
31	1053.6	13.0	7807	17	US-10-394-388A-7	Sequence 7, Appli
32	1052	13.0	7913	17	US-10-394-388A-8	Sequence 8, Appli
33	1052	13.0	13464	17	US-10-394-388A-9	Sequence 9, Appli
34	1036.2	12.8	3796	13	US-10-127-391-32	Sequence 32, Appl
35	1036.2	12.8	3796	16	US-10-241-332-32	Sequence 32, Appl
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37	983	12.1	4058	19	US-10-811-028A-5	Sequence 5, Appli
38	983	12.1	4187	19	US-10-811-028A-6	Sequence 6, Appli
39	983	12.1	4293	19	US-10-811-028A-2	Sequence 2, Appli
40	983	12.1	4332	19	US-10-811-028A-2	Sequence 2, Appli
41	983	12.1	5753	19	US-10-811-028A-3	Sequence 3, Appli
42	983	12.1	5760	19	US-10-811-028A-4	Sequence 4, Appl
43	981.8	12.1	6565	14	US-10-267-117-1	Sequence 1, Appli
44	981.8	12.1	6565	14	US-10-340-112-1	Sequence 1, Appli
45	981.8	12.1	6981	14	US-10-267-117-7	Sequence 7, Appli

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT 1
US-09-778-516A-1
Sequence 1, Application US/09778516A
Patent No. US2002010272722A1.
GENERAL INFORMATION:
APPLICANT: Lo, Wei-Yu
APPLICANT: Lo, Ming Ching
APPLICANT: Liau, Pei-Ru
TITLE OF INVENTION: LAC SHUTTLE VECTORS
FILE REFERENCE: 12875-002001
CURRENT APPLICATION NUMBER: US/09/778,516A
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: TW 89110235
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 8115
TYPE: DNA
ORGANISM: Lactobacillus plantarum
US-09-778-516A-1

Query Match 100.0%; Score 8115; DB 9; Length 8115;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 8115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy   1 GATGTACGGGCCCAGATATACGCGTTGACATTGATTATTGACTAGTTATTAATAGTAATCA 60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GATGTACGGGCCCAGATATACGCGTTGACATTGATTATTGACTAGTTATTAATAGTAATCA 60

Qy  61 ATTACGGGGGTTCATTAGTTCATAGCCCATATATATGGAGTTCCGCGTTACATTAACTACGGGTA 120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  61 ATTACGGGGGTTCATTAGTTCATAGCCCATATATATGGAGTTCCGCGTTACATTAACTACGGGTA 120
```

OM nucleic - nucleic search, using sw model

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GenCore version 5.1.6

Run on: May 28, 2005, 19:59:45 ; Search time 1161 Seconds
(without alignments)
11437.025 Million cell updates/sec

Title: US-09-778-516C-1
Perfect score: 8115
Sequence: 1 gatgtacgggccagatatac..........gggtgtcgctagcgacggtc 8115

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 81813359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/pCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1240.4	15.3	3853	3	US-08-801-092-5	Sequence 5, Appli
2	1240.4	15.3	3853	3	US-09-315-113-5	Sequence 5, Appl
3	1152.4	14.2	5314	3	US-09-479-122-27	Sequence 27, Appl
4	1152.4	14.2	5314	4	US-09-484-997-27	Sequence 27, Appl
5	1152.4	14.2	5314	4	US-09-481-355-27	Sequence 27, Appl
6	1152.4	14.2	5314	4	US-09-481-282-27	Sequence 27, Appl
7	1152.4	14.2	5314	4	US-09-455-659A-27	Sequence 27, Appl
8	1152.4	14.2	5314	4	US-09-484-996-27	Sequence 27, Appl
9	1152.4	14.2	5314	4	US-09-479-123-27	Sequence 27, Appl
10	1152.4	14.2	5314	4	US-09-484-317A-27	Sequence 27, Appl
11	1151.6	14.2	5382	3	US-09-479-122-21	Sequence 21, Appl
12	1151.6	14.2	5382	4	US-09-484-997-21	Sequence 21, Appl
13	1151.6	14.2	5382	4	US-09-481-355-21	Sequence 21, Appl
14	1151.6	14.2	5382	4	US-09-481-282-21	Sequence 21, Appl
15	1151.6	14.2	5382	4	US-09-455-659A-21	Sequence 21, Appl
16	1151.6	14.2	5382	4	US-09-484-996-21	Sequence 21, Appl
17	1151.6	14.2	5382	4	US-09-479-123-21	Sequence 21, Appl
18	1151.6	14.2	5382	3	US-09-484-317A-21	Sequence 21, Appl
19	1141.8	14.1	4644	4	US-09-479-122-19	Sequence 19, Appl
20	1141.8	14.1	4644	4	US-09-484-997-19	Sequence 19, Appl
21	1141.8	14.1	4644	3	US-09-481-355-19	Sequence 19, Appl
22	1141.8	14.1	4644	4	US-09-481-282-19	Sequence 19, Appl
23	1141.8	14.1	4644	4	US-09-455-659A-19	Sequence 19, Appl
24	1141.8	14.1	4644	4	US-09-484-996-19	Sequence 19, Appl
25	1141.8	14.1	4644	4	US-09-479-123-19	Sequence 19, Appl
26	1141.8	14.1	4644	4	US-09-484-317A-19	Sequence 19, Appl
27	1109.8	13.7	5247	3	US-09-479-122-20	Sequence 20, Appl
28	1109.8	13.7	5247	4	US-09-484-997-20	Sequence 20, Appl
29	1109.8	13.7	5247	4	US-09-481-355-20	Sequence 20, Appl
30	1109.8	13.7	5247	4	US-09-481-282-20	Sequence 20, Appl
31	1109.8	13.7	5247	4	US-09-455-659A-20	Sequence 20, Appl
32	1109.8	13.7	5247	4	US-09-484-996-20	Sequence 20, Appl
33	1109.8	13.7	5247	4	US-09-479-123-20	Sequence 20, Appl
34	1109.8	13.7	5247	4	US-09-484-317A-20	Sequence 20, Appl
35	1068.6	13.2	4026	3	US-09-315-113-19	Sequence 19, Appl
36	1068.6	13.2	4026	3	US-09-801-092-19	Sequence 19, Appl
37	1068	13.2	8705	3	US-09-760-615-7	Sequence 7, Appl
38	1053.6	13.0	4326	3	US-09-647-344A-14	Sequence 14, Appl
39	1036.2	12.8	3796	4	US-09-470-661A-32	Sequence 32, Appl
40	985.2	12.1	4276	4	US-09-721-480-1	Sequence 1, Appli
41	985.2	12.1	5128	4	US-09-721-480-2	Sequence 2, Appli
42	985.2	12.1	5459	4	US-09-721-480-4	Sequence 4, Appli
43	985.2	12.1	5882	4	US-09-721-480-6	Sequence 6, Appli
44	981.8	12.1	6253	3	US-08-893-327-15	Sequence 15, Appl
45	981.8	12.1	6280	3	US-08-893-327-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-801-092-5
Sequence 5, Application US/08801092
Patent No. 6074850
GENERAL INFORMATION:
APPLICANT: Antelman, Douglas
APPLICANT: Gregory, Richard J.
APPLICANT: Wils, Kenneth N.
TITLE OF INVENTION: Tissue Specific Expression of
TITLE OF INVENTION: Retinoblastoma Protein
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,092
FILING DATE: 14-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,517
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 016930-001020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 703-576-0300
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 3853 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 209..250
FEATURE:
NAME/KEY: CDS